

OM protein - protein search, using sw model

Run on: August 18, 2005, 09:38:49 ; Search time 79 Seconds  
 (without alignments)  
 842.061 Million cell updates/sec

Title: US-10-021-753A-2  
 Perfect score: 172  
 Sequence: 1 MIIYRDLISHDEMFSDIYKI.....EDGVTPYMIFFKDGLEMEKC 172

Scoring table: OLIGO  
 Gapop 60.0 , Gapext 60.0

Searched: 2105692 seqs, 386760381 residues

Word size : 20

Total number of hits satisfying chosen parameters: 37

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

- 1: geneseqp1980s:\*
- 2: geneseqp1990s:\*
- 3: geneseqp2000s:\*
- 4: geneseqp2001s:\*
- 5: geneseqp2002s:\*
- 6: geneseqp2003as:\*
- 7: geneseqp2003bs:\*
- 8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | %           |        | DB | ID       | Description        |
|------------|-------|-------------|--------|----|----------|--------------------|
|            |       | Query Match | Length |    |          |                    |
| 1          | 172   | 100.0       | 172    | 2  | AAR55698 | Aar55698 Tumor pro |
| 2          | 172   | 100.0       | 172    | 5  | AAU97773 | Aau97773 Human For |
| 3          | 172   | 100.0       | 172    | 6  | ABR44810 | Abr44810 Human TCP |
| 4          | 172   | 100.0       | 172    | 6  | ABU07429 | Abu07429 Protein d |
| 5          | 172   | 100.0       | 172    | 6  | ABU11888 | Abu11888 Human ABC |
| 6          | 172   | 100.0       | 172    | 7  | ADD26671 | Add26671 Human adi |
| 7          | 172   | 100.0       | 172    | 7  | ADE61268 | Ade61268 Human Pro |
| 8          | 172   | 100.0       | 172    | 7  | ADG10760 | Adg10760 Human STA |
| 9          | 172   | 100.0       | 172    | 8  | ADP82721 | Adp82721 Human for |

|    |     |       |     |   |          |          |           |
|----|-----|-------|-----|---|----------|----------|-----------|
| 10 | 172 | 100.0 | 172 | 8 | ADQ30542 | Adq30542 | Pancreas  |
| 11 | 172 | 100.0 | 172 | 8 | ABM81514 | Abm81514 | Tumour-as |
| 12 | 172 | 100.0 | 182 | 7 | ADE09075 | Ade09075 | Novel pro |
| 13 | 172 | 100.0 | 197 | 5 | ABB97354 | Abb97354 | Novel hum |
| 14 | 153 | 89.0  | 208 | 7 | ADE08040 | Ade08040 | Novel pro |
| 15 | 138 | 80.2  | 146 | 4 | ABG26035 | Abg26035 | Novel hum |
| 16 | 130 | 75.6  | 215 | 2 | AAR05882 | Aar05882 | Sequence  |
| 17 | 108 | 62.8  | 110 | 4 | ABG26036 | Abg26036 | Novel hum |
| 18 | 108 | 62.8  | 111 | 4 | AAU29787 | Aau29787 | Novel hum |
| 19 | 98  | 57.0  | 172 | 5 | AAU79211 | Aau79211 | Human tum |
| 20 | 92  | 53.5  | 108 | 4 | ABG26034 | Abg26034 | Novel hum |
| 21 | 78  | 45.3  | 172 | 5 | AAU79307 | Aau79307 | Human tra |
| 22 | 62  | 36.0  | 189 | 4 | AAU29788 | Aau29788 | Novel hum |
| 23 | 52  | 30.2  | 86  | 5 | ABP42338 | Abp42338 | Human ova |
| 24 | 52  | 30.2  | 120 | 4 | ABG26033 | Abg26033 | Novel hum |
| 25 | 35  | 20.3  | 74  | 8 | ADS12214 | Ads12214 | Human the |
| 26 | 35  | 20.3  | 191 | 4 | ABG26037 | Abg26037 | Novel hum |
| 27 | 31  | 18.0  | 172 | 5 | ABB83345 | Abb83345 | Murine TS |
| 28 | 31  | 18.0  | 172 | 5 | ABB83346 | Abb83346 | Human TSA |
| 29 | 31  | 18.0  | 172 | 5 | AAU79212 | Aau79212 | Murine tu |
| 30 | 31  | 18.0  | 172 | 5 | AAU79210 | Aau79210 | Murine tu |
| 31 | 31  | 18.0  | 172 | 7 | ADE61266 | Ade61266 | Rat Prote |
| 32 | 30  | 17.4  | 190 | 8 | ABM80805 | Abm80805 | Tumour-as |
| 33 | 26  | 15.1  | 138 | 8 | ABM81068 | Abm81068 | Tumour-as |
| 34 | 24  | 14.0  | 140 | 8 | ADR08494 | Adr08494 | Human pro |
| 35 | 21  | 12.2  | 21  | 2 | AAR60844 | Aar60844 | COSM prec |
| 36 | 21  | 12.2  | 22  | 5 | AAU97774 | Aau97774 | Synthetic |
| 37 | 20  | 11.6  | 34  | 5 | ABB83347 | Abb83347 | Murine TS |

# ALIGNMENTS

## RESULT 1

AAR55698

ID AAR55698 standard; protein; 172 AA.

XX

AC AAR55698;

XX

DT 25-MAR-2003 (revised)

DT 16-NOV-1994 (first entry)

XX

DE Tumor protein p21.

XX

KW Transcriptionally controlled tumor protein p21; TCTPp21; tumor marker;

KW ELISA; immunoassay; DNA probe; hybridization; breast cancer;

KW ovary cancer; cervix cancer; prostate cancer; colon cancer; diagnosis.

XX

OS Homo sapiens.

XX

PN WO9412881-A2.

XX

PD 09-JUN-1994.

XX

PF 26-NOV-1993; 93WO-EP003314.

XX

PR 02-DEC-1992; 92US-00990302.

**Search completed: August 18, 2005, 06:39:05**  
**Job time : 570 secs**

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OM nucleic · nucleic search, using sw model

Run on: August 18, 2005, 05:03:40 ; Search time 186 Seconds  
(without alignments)  
7301.665 Million cell updates/sec

Title: US-10-021-753A-1  
 Perfect score: 830  
 Sequence: 1 cccccgcgagcgcgctcgcg.....catttaanctatttgagag 830

Scoring table: OLIGO\_NUC  
Gapop 60.0, Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

**Word size : 20**

**Total number of hits satisfying chosen parameters:** 46

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

### Post-processing: Listing first 45 summaries

Database: Issued\_Patents\_NA.\*

- 1: /cgn2\_6p/ptodata/lnma/5A\_COMB.seq.\*
- 2: /cgn2\_6p/ptodata/lnma/5B\_COMB.seq.\*
- 3: /cgn2\_6p/ptodata/lnma/6A\_COMB.seq.\*
- 4: /cgn2\_6p/ptodata/lnma/6B\_COMB.seq.\*
- 5: /cgn2\_6p/ptodata/lnma/PTCTUS\_COMB.seq.\*
- 6: /cgn2\_6p/ptodata/lnma/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

|      | Result | Query        | ID                         | Description        |
|------|--------|--------------|----------------------------|--------------------|
| No.  | Score  | Match Length | DB ID                      |                    |
| 1    | 829    | 99.9         | 831 4 US-09-949-016-4086   | Sequence 4086, App |
| 2    | 386    | 46.5         | 446 3 US-09-397-787-96     | Sequence 96, Appl  |
| c 3  | 332    | 40.0         | 676 3 US-09-328-111-652    | Sequence 652, App  |
| c 4  | 315    | 38.0         | 333 3 US-09-035-648-15     | Sequence 15, Appl  |
| c 5  | 315    | 38.0         | 333 3 US-09-001-951-15     | Sequence 15, Appl  |
| c 6  | 315    | 38.0         | 333 3 US-08-818-829-15     | Sequence 15, Appl  |
| 7    | 279    | 33.6         | 396 4 US-09-640-173-26     | Sequence 26, Appl  |
| 8    | 279    | 33.6         | 396 4 US-09-713-550-26     | Sequence 26, Appl  |
| 9    | 279    | 33.6         | 396 4 US-09-825-294-26     | Sequence 26, Appl  |
| 10   | 279    | 33.6         | 396 4 US-09-970-966-26     | Sequence 26, Appl  |
| 11   | 242    | 29.2         | 250 3 US-09-328-111-738    | Sequence 738, App  |
| 12   | 220    | 26.5         | 7997 4 US-09-949-016-15828 | Sequence 15828, A  |
| c 13 | 119    | 14.3         | 601 4 US-09-949-016-144532 | Sequence 144532,   |
| 14   | 93     | 11.2         | 626 3 US-09-328-111-519    | Sequence 519, App  |
| c 15 | 82     | 9.9          | 82 4 US-09-724-916A-69     | Sequence 69, Appl  |
| c 16 | 82     | 9.9          | 82 4 US-09-724-916A-71     | Sequence 71, Appl  |
| c 17 | 81     | 9.8          | 601 4 US-09-949-016-144531 | Sequence 144531,   |
| c 18 | 60     | 7.2          | 81 4 US-09-621-976-11664   | Sequence 11664, A  |

|      |    |     |        |    |                       |                     |                   |
|------|----|-----|--------|----|-----------------------|---------------------|-------------------|
| 19   | 49 | 5.9 | 82     | 4  | US-09-724-916A-70     | Sequence 70, Appl   |                   |
| 20   | 49 | 5.9 | 82     | 4  | US-09-724-916A-72     | Sequence 72, Appl   |                   |
| 21   | 48 | 5.8 | 237    | 4  | US-09-471-276-313     | Sequence 313, Appl  |                   |
| c 22 | 44 | 5.3 | 84     | 4  | US-09-724-916A-83     | Sequence 83, Appl   |                   |
| c 23 | 44 | 5.3 | 84     | 4  | US-09-724-916A-84     | Sequence 84, Appl   |                   |
| 24   | 34 | 4.1 | 55     | 4  | US-09-621-976-12780   | Sequence 12780, A   |                   |
| c 25 | 29 | 3.5 | 281    | 1  | US-09-985-799-35      | Sequence 35, Appl   |                   |
| c 26 | 29 | 3.5 | 281    | 1  | US-09-985-799-127     | Sequence 127, App   |                   |
| c 27 | 29 | 3.5 | 281    | 1  | US-09-977-371-35      | Sequence 35, Appl   |                   |
| c 28 | 29 | 3.5 | 281    | 1  | US-09-977-371-127     | Sequence 127, App   |                   |
| c 29 | 29 | 3.5 | 281    | 1  | US-08-554-031-35      | Sequence 35, Appl   |                   |
| 30   | 29 | 3.5 | 281    | 1  | US-08-594-031-127     | Sequence 127, App   |                   |
| c 31 | 27 | 3.3 | 601    | 4  | US-09-949-016-157494  | Sequence 157494, A  |                   |
| c 32 | 27 | 3.3 | 601    | 4  | US-09-949-016-157601  | Sequence 157601, A  |                   |
| c 33 | 27 | 3.3 | 1261   | 76 | 4                     | US-09-949-016-16137 | Sequence 16137, A |
| c 34 | 27 | 3.3 | 1261   | 76 | 4                     | US-09-949-016-16138 | Sequence 16138, A |
| 35   | 26 | 3.1 | 349    | 1  | US-08-253-155A-14     | Sequence 14, Appl   |                   |
| 36   | 22 | 2.7 | 489    | 4  | US-09-401-064-225     | Sequence 225, Appl  |                   |
| 37   | 22 | 2.7 | 887    | 4  | US-09-016-434-58      | Sequence 58, Appl   |                   |
| c 38 | 22 | 2.7 | 874    | 70 | 4                     | US-09-949-016-15881 | Sequence 15881, A |
| c 39 | 21 | 2.5 | 25     | 4  | US-09-396-196G-72353  | Sequence 72353, A   |                   |
| c 40 | 21 | 2.5 | 25     | 4  | US-09-396-196G-72354  | Sequence 72354, A   |                   |
| c 41 | 21 | 2.5 | 25     | 4  | US-09-396-196G-123217 | Sequence 123217, A  |                   |
| c 42 | 20 | 2.4 | 25     | 4  | US-09-396-196G-72352  | Sequence 72352, A   |                   |
| c 43 | 20 | 2.4 | 7687   | 4  | US-09-949-016-5568    | Sequence 5568, Appl |                   |
| c 44 | 20 | 2.4 | 225976 | 4  | US-09-949-016-17310   | Sequence 17310, A   |                   |
| c 45 | 20 | 2.4 | 181429 | 4  | US-09-949-016-12372   | Sequence 12372, A   |                   |

## ALIGNMENTS

## RESULT 1

US-09-949-016-4086  
: Sequence 4086, Application US/09949016  
: Patent No. 6812339  
: GENERAL INFORMATION:  
: APPLICANT: VENTER, J. Craig et al.  
: TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
: FILE REFERENCE: C1001307  
: CURRENT APPLICATION NUMBER: US/09/949,016  
: CURRENT FILING DATE: 2000-04-14  
: PRIOR APPLICATION NUMBER: 60/241,755  
: PRIOR FILING DATE: 2000-10-20  
: PRIOR APPLICATION NUMBER: 60/237,768  
: PRIOR FILING DATE: 2000-10-03  
: PRIOR APPLICATION NUMBER: 60/231,498  
: PRIOR FILING DATE: 2000-09-08  
: NUMBER OF SEQ ID NOS: 207012  
: SOFTWARE: FastSeq for Windows Version 4.0  
: SEQ ID NO 4086  
: LENGTH: 831  
: TYPE: DNA  
: ORGANISM: Human  
US-09-949-016-4086

Query Match 99.9%; Score 829; DB 4; Length 831;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 829; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCCCCCGAGCGCGCGGCTCCGCTGCACCGCGCTCGCTCCGAGTTTCAGGCTCGTGCTAAGC 61  
|||||  
Ddb 3 CCCCCCGAGCGCGCGGCTCCGCTGCACCGCGCTCGCTCCGAGTTTCAGGCTCGTGCTAAGC 62  
QY 62 TAGCGCGCTCGCTCTCCCTTCACTCGCCATCATGATTATCTAACCGGGACCTCATCAGC 121

Search completed: August 18, 2005, 08:44:19  
Job time : 189 secs

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OM nucleic - nucleic search, using sw model

Run on: August 18, 2005, 06:30:09 ; Search time 2889 Seconds  
(without alignments)  
1866,543 Million cell updates/sec

Title: US-10-021-753A-1  
Perfect score: 830  
Sequence: 1 ccccccgagcgccgcgcgcg.....catttaaacatttgagag 830

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 7316285 seqs, 3248459403 residues

Word size : 20

Total number of hits satisfying chosen parameters: 709

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published\_Applications\_NA.\*  
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7: /cgn2\_6ptodata/2/pubpna/US08\_NEW\_PUB.seq.\*  
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9: /cgn2\_6ptodata/2/pubpna/US09A\_PUBCOMB.seq.\*  
10: /cgn2\_6ptodata/2/pubpna/US09B\_PUBCOMB.seq.\*  
11: /cgn2\_6ptodata/2/pubpna/US09C\_PUBCOMB.seq.\*  
12: /cgn2\_6ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*  
13: /cgn2\_6ptodata/2/pubpna/US10A\_PUBCOMB.seq.\*  
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15: /cgn2\_6ptodata/2/pubpna/US10C\_PUBCOMB.seq.\*  
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18: /cgn2\_6ptodata/2/pubpna/US10F\_PUBCOMB.seq.\*  
19: /cgn2\_6ptodata/2/pubpna/US10G\_PUBCOMB.seq.\*  
20: /cgn2\_6ptodata/2/pubpna/US10H\_PUBCOMB.seq.\*  
21: /cgn2\_6ptodata/2/pubpna/US10I\_PUBCOMB.seq.\*  
22: /cgn2\_6ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*  
23: /cgn2\_6ptodata/2/pubpna/US11A\_PUBCOMB.seq.\*  
24: /cgn2\_6ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*  
25: /cgn2\_6ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*  
26: /cgn2\_6ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

%  
Result Query SUMMARIES

| No.  | Score | Match | Length | DB | ID                   | Description       |
|------|-------|-------|--------|----|----------------------|-------------------|
| 1    | 830   | 100.0 | 830    | 9  | US-09-969-708-101    | Sequence 101, App |
| 2    | 830   | 100.0 | 830    | 14 | US-10-153-668-349    | Sequence 349, App |
| 3    | 830   | 100.0 | 830    | 16 | US-10-021-753-1      | Sequence 1, Appli |
| 4    | 830   | 100.0 | 830    | 21 | US-10-843-641A-7572  | Sequence 7572, Ap |
| 5    | 830   | 100.0 | 830    | 21 | US-10-956-157-1044   | Sequence 1044, Ap |
| 6    | 830   | 100.0 | 830    | 21 | US-10-956-157-6279   | Sequence 6279, Ap |
| 7    | 810   | 97.6  | 810    | 21 | US-10-800-322-320    | Sequence 320, App |
| c 8  | 622   | 74.9  | 823    | 20 | US-10-684-422-33     | Sequence 33, Appl |
| 9    | 590   | 71.1  | 590    | 9  | US-09-998-598-1343   | Sequence 88, Appl |
| 10   | 577   | 69.5  | 599    | 9  | US-09-919-580-88     | Sequence 88, Appl |
| 11   | 543   | 65.4  | 976    | 20 | US-10-128-558-71     | Sequence 71, Appl |
| 12   | 539   | 64.9  | 539    | 17 | US-10-242-535A-16379 | Sequence 16379, A |
| 13   | 539   | 64.9  | 539    | 18 | US-10-085-783A-16379 | Sequence 16379, A |
| 14   | 532   | 64.1  | 532    | 9  | US-09-998-598-1274   | Sequence 1274, Ap |
| 15   | 519   | 62.5  | 519    | 17 | US-10-139-794-5      | Sequence 5, Appli |
| c 16 | 519   | 62.5  | 519    | 18 | US-10-439-248-6      | Sequence 6, Appli |
| 17   | 519   | 62.5  | 577    | 9  | US-09-919-580-446    | Sequence 446, App |
| 18   | 496   | 59.8  | 506    | 9  | US-09-920-455-187    | Sequence 187, App |
| c 19 | 480   | 57.8  | 531    | 9  | US-09-920-300A-1004  | Sequence 1004, Ap |
| c 20 | 480   | 57.8  | 531    | 13 | US-10-033-528-1004   | Sequence 1004, Ap |
| c 21 | 480   | 57.8  | 531    | 16 | US-10-099-926-1004   | Sequence 1004, Ap |
| c 22 | 480   | 57.8  | 531    | 22 | US-10-961-527-1004   | Sequence 1004, Ap |
| 23   | 475   | 57.2  | 499    | 17 | US-10-242-535A-58441 | Sequence 58441, A |
| 24   | 475   | 57.2  | 499    | 18 | US-10-085-783A-58441 | Sequence 58441, A |
| 25   | 474   | 57.1  | 535    | 9  | US-09-920-300A-710   | Sequence 710, App |
| 26   | 474   | 57.1  | 535    | 13 | US-10-033-528-710    | Sequence 710, App |
| 27   | 474   | 57.1  | 535    | 16 | US-10-099-926-710    | Sequence 710, App |
| 28   | 474   | 57.1  | 535    | 22 | US-10-961-527-710    | Sequence 710, App |
| 29   | 470   | 56.6  | 521    | 9  | US-09-998-598-1025   | Sequence 1025, Ap |
| 30   | 465   | 56.0  | 465    | 17 | US-10-242-535A-36210 | Sequence 36210, A |
| 31   | 465   | 56.0  | 465    | 17 | US-10-242-535A-37978 | Sequence 37978, A |
| 32   | 465   | 56.0  | 465    | 18 | US-10-085-783A-36210 | Sequence 36210, A |
| 33   | 465   | 56.0  | 465    | 18 | US-10-085-783A-37978 | Sequence 37978, A |
| 34   | 465   | 56.0  | 703    | 11 | US-09-969-034-4221   | Sequence 4221, Ap |
| 35   | 461   | 55.5  | 490    | 9  | US-09-998-598-459    | Sequence 459, App |
| 36   | 458   | 55.2  | 508    | 10 | US-09-918-995-21311  | Sequence 21311, A |
| 37   | 457   | 55.1  | 468    | 9  | US-09-878-178-1174   | Sequence 1174, Ap |
| 38   | 457   | 55.1  | 468    | 13 | US-10-046-935-1174   | Sequence 1174, Ap |
| 39   | 457   | 55.1  | 468    | 14 | US-10-146-502-1174   | Sequence 1174, Ap |
| 40   | 456   | 54.9  | 464    | 9  | US-09-878-178-244    | Sequence 244, App |
| 41   | 456   | 54.9  | 464    | 13 | US-10-046-935-244    | Sequence 244, App |
| 42   | 456   | 54.9  | 464    | 14 | US-10-146-502-244    | Sequence 244, App |
| 43   | 453   | 54.6  | 465    | 17 | US-10-242-535A-44226 | Sequence 44226, A |
| 44   | 453   | 54.6  | 465    | 18 | US-10-085-783A-44226 | Sequence 44226, A |
| 45   | 452   | 54.5  | 502    | 10 | US-09-918-995-20920  | Sequence 20920, A |

ALIGNMENTS

RESULT 1  
US-09-969-708-101  
: Sequence 101, Application US/09969708  
: Patent No. US20020102532A1  
: GENERAL INFORMATION:  
: APPLICANT: Augustus, Meena  
: TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signature Gene  
: FILE REFERENCE: 689290-70  
: CURRENT APPLICATION NUMBER: US/09/969,708  
: CURRENT FILING DATE: 2001-10-03  
: PRIOR APPLICATION NUMBER: US/60/237,606  
: PRIOR FILING DATE: 2000-10-03  
: PRIOR APPLICATION NUMBER: US/60/237,608

Search completed: August 18, 2005, 09:32:54  
Job time : 2904 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 18, 2005, 02:13:58 ; Search time 3386 Seconds  
(without alignments)  
9330.580 Million cell updates/sec

Title: US-10-021-753A-1  
Perfect score: 830  
Sequence: 1 cccccgagcgccgctccg.....catttaacatttgagag 830

Scoring table: OLIGO\_NUC  
Gapop 60.0, Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

Word size : 20

Total number of hits satisfying chosen parameters: 13556

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST\*

- 1: gb\_est1:\*
- 2: gb\_est2:\*
- 3: gb\_hlc:\*
- 4: gb\_est3:\*
- 5: gb\_est4:\*
- 6: gb\_est5:\*
- 7: gb\_est6:\*
- 8: gb\_gss1:\*
- 9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| SUMMARIES  |                          |                    |
|------------|--------------------------|--------------------|
| %          |                          |                    |
| Result No. | Query Match Length       | Description        |
| 1          | 829 99.9 868 5 BX437546  | BX437546 BX437546  |
| 2          | 829 99.9 952 1 AL540618  | AL540618 AL540618  |
| 3          | 829 99.9 1092 3 CR618209 | CR618209 full-leng |
| 4          | 829 99.9 1096 3 CR590628 | CR590628 full-leng |
| 5          | 829 99.9 1113 3 CR615436 | CR615436 full-leng |
| 6          | 829 99.9 1116 3 CR623434 | CR623434 full-leng |
| 7          | 829 99.9 1127 3 CR619808 | CR619808 full-leng |
| 8          | 829 99.9 1132 3 CR607344 | CR607344 full-leng |
| 9          | 829 99.9 1133 3 CR620037 | CR620037 full-leng |
| 10         | 825 99.4 1090 3 CR617312 | CR617312 full-leng |
| 11         | 824 99.3 996 5 BM904232  | BM904232 AGENCOURT |
| 12         | 821 98.9 823 1 AL538559  | AL538559 AL538559  |
| 13         | 821 98.9 823 3 CR591807  | CR591807 full-leng |
| 14         | 821 98.9 825 1 AL534283  | AL534283 AL534283  |

|    |                          |                    |
|----|--------------------------|--------------------|
| 15 | 821 98.9 825 3 CR603315  | CR603315 full-leng |
| 16 | 821 98.9 829 3 CR626131  | CR626131 full-leng |
| 17 | 821 98.9 830 3 CR624492  | CR624492 full-leng |
| 18 | 821 98.9 832 3 CR600220  | CR600220 full-leng |
| 19 | 821 98.9 839 3 CR624864  | CR624864 full-leng |
| 20 | 818 98.6 818 3 CR606684  | CR606684 full-leng |
| 21 | 817 98.4 817 3 CR626086  | CR626086 full-leng |
| 22 | 812 97.8 1053 3 CR609479 | CR609479 full-leng |
| 23 | 803 96.7 826 5 BX437553  | BX437553 BX437553  |
| 24 | 802 96.6 902 6 CD247072  | CD247072 AGENCOURT |
| 25 | 799 96.3 907 5 BU857522  | BU857522 AGENCOURT |
| 26 | 796 95.9 803 7 CN386054  | CN386054 170006000 |
| 27 | 789 95.1 896 5 BQ230215  | BQ230215 AGENCOURT |
| 28 | 783 94.3 830 5 BU170315  | BU170315 AGENCOURT |
| 29 | 781 94.1 834 5 BQ672149  | BQ672149 AGENCOURT |
| 30 | 780 94.0 783 7 CN386066  | CN386066 170006001 |
| 31 | 778 93.7 909 1 AL520698  | AL520698 AL520698  |
| 32 | 778 93.7 1052 1 AL557203 | AL557203 AL557203  |
| 33 | 777 93.6 862 5 BQ228899  | BQ228899 AGENCOURT |
| 34 | 777 93.6 877 5 BQ934325  | BQ934325 AGENCOURT |
| 35 | 777 93.6 1094 4 BM463066 | BM463066 AGENCOURT |
| 36 | 776 93.5 829 4 BM801894  | BM801894 AGENCOURT |
| 37 | 775 93.4 833 4 BM479671  | BM479671 AGENCOURT |
| 38 | 774 93.3 872 5 BQ431963  | BQ431963 AGENCOURT |
| 39 | 773 93.1 834 5 BQ063102  | BQ063102 AGENCOURT |
| 40 | 772 93.0 841 5 BQ933608  | BQ933608 AGENCOURT |
| 41 | 770 92.8 826 1 AL552217  | AL552217 AL552217  |
| 42 | 770 92.8 839 5 BQ644820  | BQ644820 AGENCOURT |
| 43 | 770 92.8 845 5 BQ059130  | BQ059130 AGENCOURT |
| 44 | 770 92.8 863 5 BQ652576  | BQ652576 AGENCOURT |
| 45 | 770 92.8 888 5 BU956093  | BU956093 AGENCOURT |

ALIGNMENTS

RESULT 1  
BX437546 868 bp mRNA linear EST 04-MAY-2004  
LOCATION BX437546  
DEFINITION BX437546 Homo sapiens THYMUS Homo sapiens cDNA clone CS0CAP007TK06  
5-PRIME, mRNA sequence.  
ACCESSION BX437546  
VERSION BX437546.2 GI:47009767  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE 1 (bases 1 to 868)  
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished (2001)  
COMMENT On May 15, 2003 this sequence version replaced gi:30781584.  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with NotI and cloned  
into the NotI and EcoRV sites of the pCMVSPORT 6 vector. Library  
was not normalized. Library was constructed by Life Technologies, a  
division of Invitrogen.  
This sequence belongs to sequence cluster 6904.r  
For more information about this cluster, see  
http://www.genoscope.cns.fr/cdna?cs=CS0CAP007BF03QP1&c=6904.r.



OM protein - protein search, using sw model

Run on: August 18, 2005, 06:39:14 ; Search time 312 Seconds  
(without alignments)  
213.214 Million cell updates/sec

Title: US-10-021-753A-2  
Perfect score: 898  
Sequence: 1 MIYRDLISHDEMFSDIYKI.....EDGVTPYMIFFKQGLEMEKC 172

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04: +  
1: geneseqp1980s: +  
2: geneseqp1990s: +  
3: geneseqp2000s: +  
4: geneseqp2001s: +  
5: geneseqp2002s: +  
6: geneseqp2003as: +  
7: geneseqp2003bs: +  
8: geneseqp2004s: +

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description        |
|------------|-------|-------------|--------|-------|--------------------|
| 1          | 898   | 100.0       | 172    | 2     | AAR55698 Tumor pro |
| 2          | 898   | 100.0       | 172    | 5     | AAU97773 Human For |
| 3          | 898   | 100.0       | 172    | 6     | ABR44810 Human TCP |
| 4          | 898   | 100.0       | 172    | 6     | ABU07429 Protein d |
| 5          | 898   | 100.0       | 172    | 6     | ABU11888 Human ABC |
| 6          | 898   | 100.0       | 172    | 7     | ADD26671 Human adi |
| 7          | 898   | 100.0       | 172    | 7     | AD661268 Human pro |
| 8          | 898   | 100.0       | 172    | 7     | ADG10760 Human STA |
| 9          | 898   | 100.0       | 172    | 8     | ADP82721 Human for |
| 10         | 898   | 100.0       | 172    | 8     | ADQ30542 Pancreas  |
| 11         | 898   | 100.0       | 172    | 8     | ABM81514 Tumour-as |
| 12         | 898   | 100.0       | 182    | 7     | AD609075 Novel pro |
| 13         | 898   | 100.0       | 197    | 5     | ABB97354 Novel hum |
| 14         | 896   | 99.8        | 172    | 5     | AAU79211 Human tum |
| 15         | 872   | 97.1        | 172    | 5     | ABB83345 Murine TS |
| 16         | 872   | 97.1        | 172    | 5     | ABB83346 Human TSA |
| 17         | 872   | 97.1        | 172    | 5     | AAU79212 Murine tu |
| 18         | 872   | 97.1        | 172    | 5     | AAU79210 Murine tu |
| 19         | 870   | 96.9        | 172    | 7     | AD661266 Rat Prote |
| 20         | 870   | 96.9        | 172    | 5     | AAU79307 Human tra |
| 21         | 839   | 93.4        | 215    | 2     | AAR05882 Sequence  |
| 22         | 794   | 88.4        | 208    | 7     | AD608040 Novel pro |

|    |       |      |      |   |                    |
|----|-------|------|------|---|--------------------|
| 23 | 723   | 80.5 | 146  | 4 | ABG26035 Novel hum |
| 24 | 679   | 75.6 | 138  | 8 | ABM81068 Tumour-as |
| 25 | 673.5 | 75.0 | 189  | 4 | AAU29788 Novel hum |
| 26 | 591   | 65.8 | 140  | 8 | ADR08494 Human pro |
| 27 | 574   | 63.9 | 191  | 4 | ABG26037 Novel hum |
| 28 | 562   | 62.6 | 110  | 4 | ABG26036 Novel hum |
| 29 | 562   | 62.6 | 111  | 4 | AAU29787 Novel hum |
| 30 | 539.5 | 60.1 | 120  | 4 | ABG26033 Novel hum |
| 31 | 493   | 54.9 | 108  | 4 | ABG26034 Novel hum |
| 32 | 487   | 54.2 | 208  | 4 | AAU30283 Novel hum |
| 33 | 450   | 50.1 | 190  | 8 | ABM80805 Tumour-as |
| 34 | 384   | 42.8 | 172  | 4 | ABM60988 Drosophil |
| 35 | 380   | 42.3 | 172  | 4 | AAU28148 Novel hum |
| 36 | 380   | 42.3 | 178  | 4 | AAU28336 Novel hum |
| 37 | 371   | 41.3 | 167  | 2 | AAW48310 A flea ec |
| 38 | 304   | 33.9 | 86   | 5 | ABP42338 Human ova |
| 39 | 276   | 30.7 | 168  | 3 | AAQ41955 Arabidops |
| 40 | 276   | 30.7 | 168  | 3 | AAQ4532 Arabidops  |
| 41 | 267   | 29.7 | 168  | 7 | ADL01760 Tobacco t |
| 42 | 261.5 | 29.1 | 136  | 3 | AAQ54578 Zea mays  |
| 43 | 241   | 26.8 | 188  | 3 | AAQ35568 Arabidops |
| 44 | 210   | 23.4 | 1543 | 7 | AD608651 Novel pro |
| 45 | 208   | 23.2 | 123  | 3 | AAQ54502 Zea mays  |

ALIGNMENTS

|          |   |
|----------|---|
| RESULT 1 | AAAR55698   |
| ID       | AAAR55698 standard; protein; 172 AA.                                      |
| XX       | AC AAR55698;  |
| XX       | AC  |
| DT       | 25-MAR-2003 (revised)   |
| DT       | 16-NOV-1994 (first entry)   |
| XX       | XX  |
| DE       | Tumor protein p21.  |
| XX       | XX  |
| KW       | Transcriptionally controlled tumor protein p21; TCTPp21; tumor marker;    |
| KW       | ELISA; immunoassay; DNA probe; hybridization; breast cancer;              |
| KW       | ovary cancer; cervix cancer; prostate cancer; colon cancer; diagnosis.    |
| XX       | XX  |
| OS       | Homo sapiens.   |
| XX       | XX  |
| PN       | WO9412881-A2.   |
| XX       | XX  |
| PD       | 09-JUN-1994.  |
| XX       | XX  |
| PF       | 26-NOV-1993; 93WO-EP003314.   |
| XX       | XX  |
| PR       | 02-DEC-1992; 92US-00990302.   |
| XX       | XX  |
| PA       | (HOCH/) HOCHSTRASSER D F.   |
| PA       | (HUGH/) HUGHES G J.   |
| XX       | XX  |
| PI       | Hochstrasser DF, Hughes GJ, Appel RD;                                     |
| XX       | XX  |
| DR       | WPI; 1994-200427/24.  |
| DR       | N-PSDB; AAQ66875.   |
| XX       | XX  |
| PT       | Detection of growing cells, partic. cancer cells - by detecting a high    |
| PT       | level of translationally controlled tumour protein p21 in a patient       |
| PT       | sample.   |
| XX       | XX  |
| PS       | Disclosure; Page 19; 28pp; English.                                       |
| XX       | XX  |
| CC       | DNA coding for transcriptionally controlled tumor protein p21 (TCTPp21)   |
| CC       | was obtained by screening a cDNA library constructed in phage lambda-gt10 |
| CC       | from human breast carcinoma mRNA. TCTPp21 is a specific marker for cancer |

XX (TAKE ) TAKEDA CHEM IND LTD.  
PA  
XX  
PI Rokutan K;  
XX  
DR WPI; 2002-362309/39.  
DR N-PSDB; ABK49328.  
XX  
PT Insulin secretion-controlling agents acting on IgE-dependent histamine-  
PT releasing factors, useful in diagnosis and drugs for e.g. diabetes,  
PT obesity, edema and insulinoma.  
XX  
PS Example; Page 82-83; 89pp; Japanese.  
XX  
CC The invention relates to insulin-secretion controlling agents. IgE-  
CC dependent histamine releasing factors (IgE-dependent HRFs) such as tumour  
CC -associated protein (TCrP) are controlling factors for insulin secreted  
CC from pancreatic beta cells and are therefore useful as insulin secretion  
CC inhibitors. Substances inhibiting the effect of IgE-dependent HRFs are  
CC useful as insulin secretion promoters and preventives and remedies for  
CC diabetes. The agents are useful in diagnosis and production of drugs for  
CC treatment of disorders such as diabetes, insulin secretion failure,  
CC resistance to sugar, ketosis, acidosis, diabetic neural disorders,  
CC diabetic nephropathy, diabetic omentopathy, hyperlipaemia, sexual  
CC dysfunction, skin diseases, arthritis, bone reduction, obesity, type II  
CC diabetes, hypoglycaemia, hypertension, oedema, insulin resistance,  
CC unstable diabetes, lipotrophy, insulin allergy and insulinoma. This  
CC sequence represents human TCrP p23  
XX  
SQ Sequence 172 AA;  
  
Query Match 99.8%; Score 896; DB 5; Length 172;  
Best Local Similarity 99.4%; Pred. No. 8.5e-88;  
Matches 171; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
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DB 1 MIYRDLISHDEMFSDIYKIREIADGLCLEVEGKMSRTGNIIDSLIGNASAEPEGE 60  
  
QY 61 GTESTVITGVDIWMNHHLQETSFYKAYKKYIKDYMSIKGKLEQRPERVKPFMTGAAE 120  
DB 61 GTESTVITGVDIWMNHHLQETSFYKAYKKYIKDYMSIKGKLEQRPERVKPFMTGAAE 120  
  
QY 121 QIKHILANFNKYQFFIGENMNPDMVALLDYREDGVTPYMIFFKDGLEMEKC 172  
DB 121 QIKHILANFNKYQFFIGENMNPDMVALLDYREDGVTPYMIFFKDGLEMEKC 172  
  
RESULT 15  
ABB83345  
ID ABB83345 standard; protein; 172 AA.  
XX  
AC ABB83345;  
XX  
DT 02-SEP-2002 (first entry)  
XX  
DE Murine TSAP6 binding protein #19.  
XX  
KM Neutroprotective; cytostatic; TSAP6; apoptosis; cancer; neurodegeneration;  
KM Tumour Suppressor Activated Pathway 6; TSAP6 binding protein; tumour;  
KM murine; human.  
XX  
OS Mus musculus.  
XX  
PN WO200252274-A2.  
XX  
PD 04-JUL-2002.  
XX  
PF 24-DEC-2001; 2001WO-FR004188.  
XX

PR 26-DEC-2000; 2000FR-00017027.  
PR 18-SEP-2001; 2001WO-FR002896.  
XX  
PA (MOLE-) MOLECULAR ENGINES LAB.  
XX  
PI Amson R, Telerman A, Passer B;  
XX  
DR WPI; 2002-508914/54.  
XX  
PT Identifying compounds that inhibit binding of TSAP6 to proteins for  
PT treating cancer and neurodegeneration.  
XX  
PS Claim 1; Page 58-59; 79pp; French.  
XX  
CC The present invention relates to a method for identifying a compound (I)  
CC that inhibits binding of TSAP (Tumour Suppressor Activated Pathway) 6 to  
CC a TSAP6 binding protein. The present sequence is one such TSAP6 binding  
CC protein. (I) are useful for modulating tumour reversal and/or apoptosis  
CC for treating cancer or neurodegeneration  
XX  
SQ Sequence 172 AA;  
  
Query Match 97.1%; Score 872; DB 5; Length 172;  
Best Local Similarity 95.9%; Pred. No. 3.2e-85;  
Matches 165; Conservative 5; Mismatches 2; Indels 0; Gaps 0;  
  
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DB 1 MIYRDLISHDELFSDIYKIREIADGLCLEVEGKMSRTGAIIDSLIGNASAEPEGE 60  
  
QY 61 GTESTVITGVDIWMNHHLQETSFYKAYKKYIKDYMSIKGKLEQRPERVKPFMTGAAE 120  
DB 61 GTESTVITGVDIWMNHHLQETSFYKAYKKYIKDYMSIKGKLEQRPERVKPFMTGAAE 120  
  
QY 121 QIKHILANFNKYQFFIGENMNPDMVALLDYREDGVTPYMIFFKDGLEMEKC 172  
DB 121 QIKHILANFNKYQFFIGENMNPDMVALLDYREDGVTPYMIFFKDGLEMEKC 172  
  
Search completed: August 18, 2005, 09:38:21  
Job time : 323 secs  
  
GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.  
  
OM protein - protein search, using sw model  
  
Run on: August 18, 2005, 08:44:23 ; Search time 117 Seconds  
(without alignments)  
109.741 Million cell updates/sec  
  
Title: US-10-021-753A-2  
Perfect score: 898  
Sequence: 1 MIYRDLISHDEMFSDIYK.....EDGVTPYMIFFKDGLEMEKC 172  
  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
  
Searched: 513545 segs, 74649064 residues  
  
Total number of hits satisfying chosen parameters: 513545  
  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents\_AA:\*

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2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*

3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*

4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*

5: /cgn2\_6/ptodata/1/iaa/PCUS\_COMB.pep:\*

6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID                   | Description       |
|------------|-------|-------------|--------|----|----------------------|-------------------|
| 1          | 898   | 100.0       | 182    | 4  | US-09-949-016-9957   | Sequence 9957, Ap |
| 2          | 870   | 96.9        | 172    | 3  | US-09-311-311C-27    | Sequence 27, Appl |
| 3          | 384   | 42.8        | 191    | 4  | US-09-270-767-43182  | Sequence 43182, A |
| 4          | 371   | 41.3        | 167    | 2  | US-08-690-849-2      | Sequence 2, Appl1 |
| 5          | 371   | 41.3        | 167    | 3  | US-09-004-053-2      | Sequence 2, Appl1 |
| 6          | 347.5 | 38.7        | 196    | 4  | US-09-248-796A-14442 | Sequence 14442, A |
| 7          | 267   | 29.7        | 168    | 4  | US-09-737-300-2      | Sequence 2, Appl1 |
| 8          | 170.5 | 19.0        | 107    | 4  | US-09-270-767-39492  | Sequence 39492, A |
| 9          | 170.5 | 19.0        | 107    | 4  | US-09-270-767-54709  | Sequence 54709, A |
| 10         | 114   | 12.7        | 21     | 3  | US-08-105-904B-12    | Sequence 12, Appl |
| 11         | 114   | 12.7        | 21     | 3  | US-08-114-877A-12    | Sequence 12, Appl |
| 12         | 107   | 11.9        | 21     | 3  | US-08-537-928-12     | Sequence 12, Appl |
| 13         | 107   | 11.9        | 21     | 4  | US-09-633-269-12     | Sequence 12, Appl |
| 14         | 85    | 9.5         | 332    | 4  | US-09-248-796A-15783 | Sequence 15783, A |
| 15         | 82    | 9.1         | 459    | 4  | US-09-489-039A-7416  | Sequence 7416, Ap |
| 16         | 81.5  | 9.1         | 570    | 4  | US-09-949-016-6071   | Sequence 6071, Ap |
| 17         | 81.5  | 9.1         | 593    | 4  | US-09-949-016-10192  | Sequence 10192, A |
| 18         | 81.5  | 9.1         | 759    | 4  | US-09-328-352-7650   | Sequence 7650, Ap |
| 19         | 81.5  | 9.1         | 1023   | 4  | US-09-762-724-14     | Sequence 14, Appl |
| 20         | 80.5  | 9.0         | 1017   | 4  | US-09-762-724-12     | Sequence 12, Appl |
| 21         | 80    | 8.9         | 16     | 2  | US-08-658-639-2      | Sequence 2, Appl1 |
| 22         | 80    | 8.9         | 16     | 3  | US-08-944-604-2      | Sequence 2, Appl1 |
| 23         | 79.5  | 8.9         | 1391   | 4  | US-10-080-505-11     | Sequence 11, Appl |
| 24         | 79.5  | 8.9         | 1391   | 4  | US-10-080-505-15     | Sequence 15, Appl |
| 25         | 79    | 8.8         | 449    | 4  | US-09-603-208A-42    | Sequence 42, Appl |
| 26         | 78    | 8.7         | 256    | 3  | US-09-134-001C-5211  | Sequence 5211, Ap |
| 27         | 77.5  | 8.6         | 331    | 4  | US-09-744-072-2      | Sequence 2, Appl1 |
| 28         | 77.5  | 8.6         | 1529   | 4  | US-09-107-433-4771   | Sequence 4771, Ap |
| 29         | 77.5  | 8.6         | 2138   | 4  | US-09-583-110-5274   | Sequence 5274, Ap |
| 30         | 77    | 8.6         | 438    | 4  | US-09-589-510-10     | Sequence 10, Appl |
| 31         | 76    | 8.5         | 251    | 4  | US-09-107-532A-5242  | Sequence 5242, Ap |
| 32         | 76    | 8.5         | 1007   | 3  | US-08-961-083-216    | Sequence 216, App |
| 33         | 76    | 8.5         | 1007   | 4  | US-09-536-784-216    | Sequence 216, App |
| 34         | 75.5  | 8.4         | 231    | 4  | US-08-961-083-176    | Sequence 176, App |
| 35         | 75.5  | 8.4         | 231    | 4  | US-09-536-784-176    | Sequence 176, App |
| 36         | 75.5  | 8.4         | 511    | 4  | US-09-248-796A-16380 | Sequence 16380, A |
| 37         | 75.5  | 8.4         | 872    | 1  | US-08-451-715A-8     | Sequence 8, Appl1 |
| 38         | 75.5  | 8.4         | 1027   | 4  | US-09-762-724-8      | Sequence 8, Appl1 |
| 39         | 75    | 8.4         | 231    | 2  | US-08-969-721-8      | Sequence 8, Appl1 |
| 40         | 75    | 8.4         | 328    | 4  | US-09-902-540-10796  | Sequence 10796, A |
| 41         | 75    | 8.4         | 492    | 4  | US-09-991-258-5      | Sequence 5, Appl1 |
| 42         | 75    | 8.4         | 642    | 4  | US-09-248-796A-15380 | Sequence 15380, A |
| 43         | 75    | 8.4         | 890    | 4  | US-09-849-602-19     | Sequence 19, Appl |
| 44         | 74.5  | 8.3         | 526    | 4  | US-09-248-796A-16081 | Sequence 16081, A |
| 45         | 74.5  | 8.3         | 587    | 4  | US-09-328-352-8096   | Sequence 8096, Ap |

ALIGNMENTS

RESULT 1

US-09-949-016-9957

; Sequence 9957, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: C1001307

; CURRENT APPLICATION NUMBER: US/09/949, 016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241, 755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237, 768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231, 498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 9957

; LENGTH: 182

; TYPE: PRT

; ORGANISM: Human

US-09-949-016-9957

Query Match 100.0%; Score 898; DB 4; Length 182;

Best Local Similarity 100.0%; Pred. No. 8.3e-88;

Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIYRDLISHDENFSDIYKIREIADGLCLEVEGKMSRTEGIDSLIGNASAEPEGE 60

Db 11 MIYRDLISHDENFSDIYKIREIADGLCLEVEGKMSRTEGIDSLIGNASAEPEGE 70

QY 61 GTESTVITGVDDIYVNHHLQETSFTKEAYKKYIKDYMSIKGLLEQRPERRKPEMTGAAR 120

Db 71 GTESTVITGVDDIYVNHHLQETSFTKEAYKKYIKDYMSIKGLLEQRPERRKPEMTGAAR 130

QY 121 QIKHILANFNKYOFFIGENMNPDMVALLDYREDGVTPYMIFFKDLMEK 172

Db 131 QIKHILANFNKYOFFIGENMNPDMVALLDYREDGVTPYMIFFKDLMEK 182

RESULT 2

US-09-311-311C-27

; Sequence 27, Application US/09311311C

; Patent No. 6358738

; GENERAL INFORMATION:

; APPLICANT: Erikson, et al.

; TITLE OF INVENTION: POLO BOX THERAPEUTIC COMPOSITIONS,

; TITLE OF INVENTION: METHODS, AND USES THEREFOR

; FILE REFERENCE: 1874/117

; CURRENT APPLICATION NUMBER: US/09/311,311C

; CURRENT FILING DATE: 1999-05-13

; PRIOR APPLICATION NUMBER: US 60/085,296

; PRIOR FILING DATE: 1998-05-13

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 27

; LENGTH: 172

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: DOMAIN

; LOCATION: (1)..(172)

; OTHER INFORMATION: TCTP/23 protein

US-09-311-311C-27

Query Match 96.9%; Score 870; DB 3; Length 172;

Best Local Similarity 97.7%; Pred. No. 7.4e-85;

Matches 168; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MIYRDLISHDENFSDIYKIREIADGLCLEVEGKMSRTEGIDSLIGNASAEPEGE 60

|||||



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Query Match          9.1%; Score 82; DB 4; Length 459;
Best Local Similarity 22.0%; Pred. No. 3;
Matches 39; Conservative 27; Mismatches 43; Indels 68; Gaps 7;

Oy 6 DLISHDEMFSDIKYIREIADGL-----CLEVEGKVRSRREGNIDSLIGNASAE 55
   |::: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 181 DFVANPQVDPVYLERGRYLVGLGHGCACTPRSLTMQKALSESBG--DDYLAGSNAPID 238
   |::: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Oy 56 G-----PEGEGT-----ESTVITGVDIYNNHLDQETSTFKEAYK 89
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Db 239 GWASSSLRGENRDLGTWSEAELEFLKTGRNDKSVFEGGMSDVYEHSLQ----- 288
   | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | |

Oy 90 KYIYD-----YKSIKIGKLEQRPERYKPFM-----TGAAEQIKHILA 127
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 289 -YISDDDTISARIYLIKSLPPRGKQTPAPYEDSVAKDLMKGNDSKTGAALYYDNCAL 344
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

Search completed: August 18, 2005, 09:48:27
Job time : 123 secs

                                GenCore version 5.1.6
                                Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on:      August 18, 2005, 09:38:35 ; Search time 491 Seconds
              (without alignments)
              137.175 Million cell updates/sec

Title:       US-10-021-753A-2
Perfect score: 898
Sequence:    1 MIIVYDLISHDEMFSDIKYI.....EDGVTPYMIFFKDGLEMEKC 172

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:      1759131 seqs, 391586102 residues

Total number of hits satisfying chosen parameters: 1759131

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

Database :      Published Applications_Aa.*
               1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
               2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
               3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
               4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
               5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
               6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
               7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
               8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
               9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
              10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
              11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
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              13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
              14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
              15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
              16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
              17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
              18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
              19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
              20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*

```

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID          | Description         |
|------------|-------|-------------|--------|----|-------------|---------------------|
| 1          | 898   | 100.0       | 172    | 1  | TCTP_HUMAN  | P13693 homo sapien  |
| 2          | 898   | 100.0       | 172    | 1  | TCTP_PIG    | P61288 sus scrofa   |
| 3          | 884   | 98.4        | 172    | 1  | TCTP_RABBIT | P43348 oryctolagus  |
| 4          | 872   | 97.1        | 172    | 1  | TCTP_MOUSE  | P63028 mus musculu  |
| 5          | 872   | 97.1        | 172    | 1  | TCTP_RAT    | P63029 rattus norv  |
| 6          | 872   | 97.1        | 172    | 1  | TCTP_MOUSE  | P63028 mus musculu  |
| 7          | 831   | 92.5        | 172    | 1  | TCTP_CHICK  | P43347 gallus gall  |
| 8          | 803   | 89.4        | 155    | 2  | Q862G3      | Q862G3 bos taurus   |
| 9          | 723   | 80.5        | 138    | 2  | Q8T8K7      | Q8T8K7 homo sapien  |
| 10         | 643.5 | 71.7        | 173    | 1  | FKG2_HUMAN  | Q9ha06 homo sapien  |
| 11         | 635   | 70.7        | 172    | 2  | Q66JCS      | Q66JCS xenopus tro  |
| 12         | 632.5 | 70.4        | 171    | 1  | TCTP_LABRO  | Q98sj7 labeo rohit  |
| 13         | 628.5 | 70.0        | 171    | 1  | TCTP_BRARE  | Q9d9k4 brachydanio  |
| 14         | 627   | 69.8        | 172    | 2  | Q7ZYF2      | Q7zyf2 xenopus lae  |
| 15         | 620.5 | 69.1        | 171    | 2  | Q7ZUG2      | Q7zug2 brachydanio  |
| 16         | 602   | 67.0        | 117    | 2  | Q862H4      | Q862H4 bos taurus   |
| 17         | 591   | 65.8        | 140    | 2  | Q6ZT11      | Q6ztl1 homo sapien  |
| 18         | 581   | 64.7        | 170    | 2  | Q6XSH4      | Q6xsh4 lateolabrax  |
| 19         | 572   | 63.7        | 114    | 2  | Q862L1      | Q862L1 bos taurus   |
| 20         | 502   | 55.9        | 95     | 2  | Q862X2      | Q862X2 bos taurus   |
| 21         | 471.5 | 52.5        | 169    | 1  | TCTP_BRABE  | Q95vy2 branchiosto  |
| 22         | 470   | 52.3        | 92     | 2  | Q862N1      | Q862N1 bos taurus   |
| 23         | 468   | 52.1        | 88     | 2  | Q862Y4      | Q862Y4 bos taurus   |
| 24         | 430   | 47.9        | 114    | 2  | Q9UP43      | Q9up43 homo sapien  |
| 25         | 412   | 45.9        | 168    | 1  | TCTP_SCHPO  | Q10344 schizosacch  |
| 26         | 409.5 | 45.6        | 167    | 2  | Q6CAG1      | Q6c4g1 yarrowia li  |
| 27         | 392   | 43.7        | 172    | 2  | Q7SVN3      | Q7svn3 bombyx mori  |
| 28         | 387   | 43.1        | 172    | 2  | Q6XIN1      | Q6xin1 drosophila   |
| 29         | 384   | 42.8        | 172    | 1  | TCTP_DROME  | Q9vgs2 drosophila   |
| 30         | 372.5 | 41.5        | 412    | 2  | Q9NWX1      | Q9nwx1 homo sapien  |
| 31         | 371.5 | 41.4        | 185    | 2  | Q7QCK2      | Q7qck2 anopheles g  |
| 32         | 366.5 | 40.8        | 167    | 2  | Q6CTH3      | Q6cth3 kluveromyc   |
| 33         | 362.5 | 40.4        | 167    | 2  | Q6FKB6      | Q6fkb6 candida gla  |
| 34         | 361.5 | 40.3        | 167    | 1  | TCTP_LUMRU  | O18477 lumbricus r  |
| 35         | 358.5 | 39.9        | 167    | 1  | TCTP_YEAST  | P35691 saccharomyc  |
| 36         | 357   | 39.8        | 170    | 2  | Q7RYV5      | Q7ryv5 neurospora   |
| 37         | 355.5 | 39.6        | 169    | 1  | TCTP_SCHJA  | P91800 schistosoma  |
| 38         | 347.5 | 38.7        | 167    | 2  | Q6BP09      | Q6bp09 debaromyce   |
| 39         | 333   | 37.1        | 172    | 2  | Q6RJR2      | Q6rjr2 tigrilopus j |
| 40         | 329   | 36.6        | 64     | 2  | Q86YH5      | Q86yh5 homo sapien  |
| 41         | 326   | 36.3        | 166    | 1  | TCTP_SCHMA  | Q95wa2 schistosoma  |
| 42         | 325   | 36.2        | 147    | 2  | Q6XHY0      | Q6xhy0 drosophila   |
| 43         | 322   | 35.9        | 168    | 2  | Q86GR2      | Q86gr2 penaeus mon  |
| 44         | 319.5 | 35.6        | 173    | 2  | Q8T9S3      | Q8t9s3 dermaceator  |
| 45         | 307.5 | 34.2        | 167    | 1  | TCTP_MEDSA  | P28014 medicago sa  |

ALIGNMENTS

RESULT 1  
TCTP\_HUMAN STANDARD; PRT; 172 AA.  
AC P13693; Q6YLS2; Q7Z4J4; Q96EE2; Q9UC70;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-JAN-1990 (Rel. 13, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Translationally controlled tumor protein (TCTP) (p23) (Histamine-releasing factor) (HRF).

GN Name=TPP1;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=90045959; PubMed=2813067;  
RA Gross B., Gaestel M., Boehm H., Bietke H.;  
RT "cDNA sequence coding for a translationally controlled human tumor protein.";  
RL Nucleic Acids Res. 17:8367-8367(1989).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Thiele H.;  
RL Thesis (2000), Humboldt-University Berlin, Germany.  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Gnanasekar M., Ramaswamy K.;  
RT "Cloning and characterization of TCTP from human eosinophils.";  
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RA Gao T.H., Duan F.L., Zhu W.L.;  
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE FROM N.A.  
RA Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;  
RT "Cloning of human full open reading frames in Gateway(TM) system entry vector (pDONR201)." ;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung, and Placenta;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences." ;  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [7]  
RP SEQUENCE OF 1-10.  
RC TISSUE=Liver;  
RX MEDLINE=93162045; PubMed=1286669;  
RA Hochstrasser D.F., Frutiger S., Paquet N., Bairoch A., Ravier F.,  
RA Pasquali C., Sanchez J.-C., Tissot J.-D., Bjellqvist B., Vargaa R.,  
RA Appel R.D., Hughes G.J.;  
RT "Human liver protein map: a reference database established by microsequencing and gel comparison." ;  
RL Electrophoresis 13:992-1001(1992).  
RN [8]  
RP SEQUENCE OF 1-4; 22-31; 39-45 AND 103-109.  
RC TISSUE=Keratinocytes;  
RX MEDLINE=93162043; PubMed=1286667;  
RA Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E.,

; TITLE OF INVENTION: Novel Nucleic Acids and
; FILE REFERENCE: Polypeptides
; CURRENT APPLICATION NUMBER: US/10/128,558
; CURRENT FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: US 60/339,453
; PRIOR FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: PCT/US01/03800
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 09/515,126
; PRIOR FILING DATE: 2000-02-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 412
; SOFTWARE: pt\_fl\_genes Version 6.0
; SEQ ID NO 378
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; ORGANISM: Homo sapiens
US-10-128-558-378

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Matches 109; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIIYRDLISHDEMFSDIYKIEIADGICLVEGKMSRTEGNIDDSLIGNASAEPPGE 60
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61 GTESTVITGVDIVMNNHHLQETSFTKEAYKKYIKDYMSIKGKLEEQRPDR 110
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RESULT 15
US-10-425-115-319995
; Sequence 319995, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 319995
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577\_54903C.1.pep
US-10-425-115-319995

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QY 126 LANENKVOFFIGENMNPDMVALLDYREDGVTPYMIFFKDGLEME 170
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Db 61 LANENKVOFFIGENMNPDMVALLDYREDGVTPYMIFFKDGLEME 105

Search completed: August 18, 2005, 09:56:41
Job time : 493 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2005, 08:41:19 ; Search time 71 Seconds
(without alignments)
233.088 Million cell updates/sec

Title: US-10-021-753A-2
Perfect score: 898
Sequence: 1 MIIYRDLISHDEMFSDIYKIEIADGICLVEGKMSRTEGNIDDSLIGNASAEPPGE 60
.....EDGVTPYMIFFKDGLEMEKC 172

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR\_79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Query length | DB ID    | Description        |
|------------|-------|-------------|--------------|----------|--------------------|
| 1          | 898   | 100.0       | 172          | 1 S06590 | IgE-dependent hist |
| 2          | 872   | 97.1        | 172          | 1 S00775 | IgE-dependent hist |
| 3          | 862   | 96.0        | 172          | 1 A38956 | IgE-dependent hist |
| 4          | 831   | 92.5        | 172          | 1 A38960 | IgE-dependent hist |
| 5          | 412   | 45.9        | 168          | 2 S67445 | IgE-dependent hist |
| 6          | 358.5 | 39.9        | 167          | 1 S37878 | IgE-dependent hist |
| 7          | 307.5 | 34.2        | 167          | 2 T09686 | TCTP protein homol |
| 8          | 302.5 | 33.7        | 167          | 2 T06567 | IgE-dependent hist |
| 9          | 291   | 32.4        | 168          | 1 A38958 | IgE-dependent hist |
| 10         | 278.5 | 31.0        | 157          | 2 S22489 | IgE-dependent hist |
| 11         | 274   | 30.5        | 168          | 1 A38959 | IgE-dependent hist |

|    |       |      |      |   |        |                     |
|----|-------|------|------|---|--------|---------------------|
| 12 | 256.5 | 28.6 | 181  | 2 | T21352 | hypothetical prote  |
| 13 | 92.5  | 10.3 | 537  | 2 | T27612 | hypothetical prote  |
| 14 | 90.5  | 10.1 | 870  | 2 | G81348 | valine-tRNA ligase  |
| 15 | 87.5  | 9.7  | 488  | 2 | T10258 | gag polyprotein ho  |
| 16 | 87    | 9.7  | 572  | 1 | ERBP22 | DNA-directed DNA p  |
| 17 | 87    | 9.7  | 575  | 1 | ERBP29 | Ulp protein - mou   |
| 18 | 86.5  | 9.6  | 570  | 2 | S55525 | 1-phosphatidylinos  |
| 19 | 85    | 9.5  | 329  | 2 | A33493 | hypothetical prote  |
| 20 | 85    | 9.5  | 1173 | 2 | T25985 | 1-phosphatidylinos  |
| 21 | 84    | 9.4  | 329  | 2 | A30760 | hypothetical prote  |
| 22 | 84    | 9.4  | 1787 | 2 | T20160 | atp synthase beta   |
| 23 | 83.5  | 9.3  | 468  | 2 | B90568 | hypothetical prote  |
| 24 | 83    | 9.2  | 496  | 2 | T46356 | hypothetical prote  |
| 25 | 82.5  | 9.2  | 598  | 2 | H69011 | conserved hypothec  |
| 26 | 81.5  | 9.1  | 390  | 2 | A64549 | dihydropyrimidinas  |
| 27 | 81.5  | 9.1  | 570  | 2 | JC5318 | major surface glyco |
| 28 | 81.5  | 9.1  | 1022 | 2 | T30543 | ladder protein - C  |
| 29 | 81    | 9.0  | 1198 | 2 | T42223 | H+/K+-exchanging A  |
| 30 | 80.5  | 9.0  | 673  | 2 | T44079 | hypothetical prote  |
| 31 | 80.5  | 9.0  | 673  | 2 | B69766 | major surface glyco |
| 32 | 80.5  | 9.0  | 1017 | 2 | T30542 | hypothetical prote  |
| 33 | 80    | 8.9  | 323  | 2 | A86184 | plasmid replicatio  |
| 34 | 80    | 8.9  | 1073 | 1 | T08228 | transcription regu  |
| 35 | 79    | 8.8  | 300  | 2 | AF1115 | hypothetical prote  |
| 36 | 79    | 8.8  | 341  | 2 | S31236 | hypothetical prote  |
| 37 | 79    | 8.8  | 745  | 2 | S49155 | heat shock protein  |
| 38 | 78.5  | 8.7  | 266  | 2 | T41094 | very hypothetical   |
| 39 | 78.5  | 8.7  | 304  | 2 | G82940 | hypothetical prote  |
| 40 | 78.5  | 8.7  | 872  | 2 | E71852 | valine-tRNA ligase  |
| 41 | 78.5  | 8.7  | 874  | 2 | A64664 | galactosamine-cont  |
| 42 | 78.5  | 8.7  | 900  | 2 | B69631 | hypothetical prote  |
| 43 | 78    | 8.7  | 441  | 2 | T25947 | hypothetical prote  |
| 44 | 78    | 8.7  | 469  | 2 | B70201 | gag polyprotein -   |
| 45 | 78    | 8.7  | 501  | 2 | S54377 |                     |

ALIGNMENTS

RESULT 1  
S06590  
Igf-dependent histamine-releasing factor - human  
N:Alternate names: 21K tumor protein; tumor-associated protein  
C:Species: Homo sapiens (man)  
C>Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: S06590; A43082; F33178  
R:Gross, B.; Gaestel, M.; Boehm, H.; Bielka, H.  
Nucleic Acids Res. 17, 8367, 1989  
A:Title: cDNA sequence coding for a translationally controlled human tumor protein.  
A:Reference number: S06590; MUID:90045959; PMID:2813067  
A:Accession: S06590  
A:Molecule type: mRNA  
A:Residues: 1-172 <GRO>  
A:Cross-references: UNIPROT:P13693; EMBL:X16064; MID:g37495; PIDN:CAA34200.1; PID:g37496  
R:MacDonald, S.M.; Rafnar, T.; Langdon, J.; Lichtenstein, L.M.  
Science 269, 688-690, 1995  
A:Title: Molecular identification of an IgE-dependent histamine-releasing factor.  
A:Reference number: A43082; MUID:95350660; PMID:7542803  
A:Accession: A43082  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-18 <MAC>  
R:Ward, L.D.; Hong, J.; Whitehead, R.H.; Simpson, R.J.  
Electrophoresis 11, 883-891, 1990  
A:Title: Development of a database of amino acid sequences for human colon carcinoma proteins separated by two-dimensional polyacrylamide gel electrophoresis.  
A:Reference number: A33178; MUID:91176935; PMID:2079031  
A:Accession: F33178  
A:Status: preliminary

A:Molecule type: protein  
A:Residues: 1-18 <MAR>  
C:Genetics:  
A:Gene: GDB:TPT1; TCTP  
A:Cross-references: GDB:134697  
A:Map position: 13q14.3-13q14.3  
C:Superfamily: IgE-dependent histamine-releasing factor  
C:Keywords: lymphocyte

Query Match 100.0%; Score 898; DB 1; Length 172;  
Best Local Similarity 100.0%; Pred. No. 7.6e-69;  
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

|    |     |  |     |
|----|-----|--|-----|
| QY | 1   | MIYYRDLISHDEMFSDIYKIREIADGICLVEEGKMVSRTGNIIDSLIGNASAEPEGE    | 60  |
| DB | 1   | MIYYRDLISHDEMFSDIYKIREIADGICLVEEGKMVSRTGNIIDSLIGNASAEPEGE    | 60  |
| QY | 61  | GTESTVITGVDIVMNNHHQETSTFTEKAYKKYIKDYMKSIKGLBEQRPERVKPFMTGALE | 120 |
| DB | 61  | GTESTVITGVDIVMNNHHQETSTFTEKAYKKYIKDYMKSIKGLBEQRPERVKPFMTGALE | 120 |
| QY | 121 | QIKHIIANFNKYQFFIGENMNPDMVALLDYREDGVTPTMIFFRDGLEMEKC          | 172 |
| DB | 121 | QIKHIIANFNKYQFFIGENMNPDMVALLDYREDGVTPTMIFFRDGLEMEKC          | 172 |

RESULT 2  
S00775  
Igf-dependent histamine-releasing factor - mouse  
N:Alternate names: 21K tumor protein; tumor-associated protein  
C:Species: Mus musculus (house mouse)  
C>Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: S00775  
R:Chitpatima, S.T.; Makrides, S.; Bandyopadhyay, R.; Braverman, G.  
Nucleic Acids Res. 16, 2350, 1988  
A:Title: Nucleotide sequence of a major messenger RNA for a 21 kilodalton polypeptide that is under translational control in mouse tumor cells.  
A:Reference number: S00775; MUID:88189840; PMID:3357792  
A:Accession: S00775  
A:Molecule type: mRNA  
A:Residues: 1-172 <CHI>  
A:Cross-references: UNIPROT:P14701; EMBL:X06407; MID:g52848; PIDN:CAA29697.1; PID:g52849  
C:Superfamily: IgE-dependent histamine-releasing factor  
C:Keywords: lymphocyte

Query Match 97.1%; Score 872; DB 1; Length 172;  
Best Local Similarity 95.9%; Pred. No. 1.2e-66;  
Matches 165; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

|    |     |  |     |
|----|-----|--|-----|
| QY | 1   | MIYYRDLISHDEMFSDIYKIREIADGICLVEEGKMVSRTGNIIDSLIGNASAEPEGE    | 60  |
| DB | 1   | MIYYRDLISHDEMFSDIYKIREIADGICLVEEGKMVSRTGAIIDSLIGNASAEPEGE    | 60  |
| QY | 61  | GTESTVITGVDIVMNNHHQETSTFTEKAYKKYIKDYMKSIKGLBEQRPERVKPFMTGALE | 120 |
| DB | 61  | GTESTVITGVDIVMNNHHQETSTFTEKAYKKYIKDYMKSIKGLBEQRPERVKPFMTGALE | 120 |
| QY | 121 | QIKHIIANFNKYQFFIGENMNPDMVALLDYREDGVTPTMIFFRDGLEMEKC          | 172 |
| DB | 121 | QIKHIIANFNKYQFFIGENMNPDMVALLDYREDGVTPTMIFFRDGLEMEKC          | 172 |

RESULT 3  
A38956  
Igf-dependent histamine-releasing factor - rabbit  
N:Alternate names: 21K tumor protein; tumor-associated protein  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C>Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: A38956